

SEQUENCE LISTING

<110> Bufo, Bernd
 Hofmann, Thomas
 Krautwurst, Dietmar
 Kuhn, Christina
 Meyerhof, Wolfgang

<120> Bitter taste receptors

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<140> US 10/528630

<141> 2005-03-22

<150> PCT/EP2003/010691

<151> 2003-09-25

<150> US 60/413298

<151> 2002-09-25

<160> 52

<170> PatentIn version 3.2

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<213> Homo sapiens

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Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
 35 40 45

Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
 50 55 60

Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
 65 70 75 80

Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
 85 90 95

Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
 100 105 110

Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
 115 120 125

Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
 130 135 140

Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
 145 150 155 160

Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
 165 170 175

Asn Asn Asn Thr Arg Leu Asn Trp Gln Asn Lys Asp Leu Asn Leu Phe
 180 185 190

Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
 195 200 205

Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
 210 215 220

Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
 225 230 235 240

Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
 245 250 255

Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
 260 265 270

Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
 275 280 285

Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
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Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
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Val Arg Ala Asp His Lys Ala Asp Ser Arg Thr Leu Cys
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 20 25 30

Leu Ile Thr Leu Ile Leu Ala Val Leu Leu Ala Glu Tyr Leu Ile Gly
 35 40 45

Ile Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val
 50 55 60

Gln Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser
 65 70 75 80

Val Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile
 85 90 95

Ser Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala
 100 105 110

Phe Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala
 115 120 125

Ala Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr
 130 135 140

Pro Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp
 145 150 155 160

Leu Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys
 165 170 175

Ile Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser
 180 185 190

Ser Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly
 195 200 205

Leu Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe
 210 215 220

Ile Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu
 225 230 235 240


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Lys Val Thr Phe Thr Leu Val Val Ser Gly Ile Glu Cys Ile Thr Gly
          20           25           30

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Ile Leu Gly Ser Gly Phe Ile Thr Ala Ile Tyr Gly Ala Glu Trp Ala
          35           40           45

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Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
          50           55           60

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Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
65           70           75           80

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Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
          85           90           95

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Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
          100          105          110

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Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
          115          120          125

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Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
          130          135          140

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Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu
 145 150 155 160

Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
 165 170 175

Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
 180 185 190

Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
 195 200 205

Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
 210 215 220

Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
 225 230 235 240

Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
 245 250 255

Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
 260 265 270

Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
 275 280 285

Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
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Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
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Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
20           25           30

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Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
35           40           45

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Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
50           55           60

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His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
 65 70 75 80

Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
 85 90 95

Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile Ala
 100 105 110

Asn Ile Thr His Ser Thr Phe Leu Trp Leu Lys Trp Arg Phe Leu Gly
 115 120 125

Trp Val Pro Trp Leu Leu Leu Gly Ser Val Leu Ile Ser Phe Ile Ile
 130 135 140

Thr Leu Leu Phe Phe Trp Val Asn Tyr Pro Val Tyr Gln Glu Phe Leu
 145 150 155 160

Ile Arg Lys Phe Ser Gly Asn Met Thr Tyr Lys Trp Asn Thr Arg Ile
 165 170 175

Glu Thr Tyr Tyr Phe Pro Ser Leu Lys Leu Val Ile Trp Ser Ile Pro
 180 185 190

Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
 195 200 205

Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
 210 215 220

Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
 225 230 235 240

Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
 245 250 255

Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
 260 265 270

Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
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Trp Val Ala
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Ile Glu Ser Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Asn Ser Val Glu Val
 65 70 75 80

Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
 85 90 95

Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125

Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
 130 135 140

Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Asn
 165 170 175

Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190

Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu Arg Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

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Ile Glu Arg Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
50 55 60

Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
65 70 75 80

Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
115 120 125

Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
130 135 140

Phe Val Ile Asn Met Lys Glu Ile Val Arg Thr Lys Glu Tyr Glu Gly
145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Val Tyr Leu Ser Asp
165 170 175

Ala Thr Val Thr Thr Leu Gly Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190

Leu Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Phe Phe Leu Leu Leu Cys Ala Val
 225 230 235 240

Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255

Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270

Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Arg Gln Val Arg Tyr Trp Val Lys Gly Glu
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Lys Pro Ser Ser Pro
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20 25 30

Thr Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Val
35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Cys Ser Val Glu Leu
65 70 75 80

Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Thr Gly His Phe Ser Asn
85 90 95

Trp Pro Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Phe Leu Arg Leu Lys Arg Arg Val Lys Ser Val
115 120 125

Ile Leu Val Val Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
 130 135 140

Phe Val Val Asn Met Asn Gln Ile Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Arg Arg Ala Met Tyr Leu Ser Asp
 165 170 175

Thr Thr Val Thr Met Leu Ala Asn Leu Val Pro Phe Thr Val Thr Leu
 180 185 190

Ile Ser Phe Leu Leu Leu Val Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Val Leu Gln Thr Val Ile Ser Phe Phe Leu Leu Arg Ala Ile
 225 230 235 240

Tyr Phe Val Ser Val Ile Ile Ser Val Trp Ser Phe Lys Asn Leu Glu
 245 250 255

Asn Lys Pro Val Phe Met Phe Cys Gln Ala Ile Gly Phe Ser Cys Ser
 260 265 270

Ser Ala His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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Thr Tyr Leu Ser Val Leu Trp Gln Met Arg Tyr
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<210> 15
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<400> 15

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Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
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Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
          20           25           30

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Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
          35           40           45

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Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Val Leu
          50           55           60

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Asn Trp Tyr Ala Thr Glu Leu Asn Pro Ala Phe Asn Ser Ile Glu Val
65           70           75           80

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Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Ile Asn His Phe Ser Asn
          85           90           95

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Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
 130 135 140

Phe Val Ile Asn Met Asn Gln Ile Ile Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr Leu Ser Asn
 165 170 175

Thr Thr Val Thr Ile Leu Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190

Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Met Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

Tyr Phe Leu Ser Ile Ile Met Ser Val Trp Ser Phe Glu Ser Leu Glu
 245 250 255

Asn Lys Pro Val Phe Met Phe Cys Glu Ala Ile Ala Phe Ser Tyr Pro
 260 265 270

Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Met Arg Tyr
 290 295

<210> 16
 <211> 897

<212> DNA

<213> Homo sapiens

<400> 16

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<210> 17

<211> 308

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<213> Homo sapiens

<400> 17

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Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Ile
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Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20           25           30

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Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Val Asp Gln Ile Leu
35           40           45

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Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
50           55           60

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His Trp Tyr Ala Thr Gln Leu Asn Pro Ala Phe Tyr Ser Val Glu Val
65 70 75 80

Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Thr Asn His Phe Ser Ser
85 90 95

Trp Leu Ala Thr Ser Leu Ser Met Phe Tyr Leu Leu Arg Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Phe Leu Arg Ile Lys Arg Arg Val Lys Ser Val
115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
130 135 140

Phe Val Ile Asn Met Asp Glu Thr Val Trp Thr Lys Glu Tyr Glu Gly
145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr His Ser Asn
165 170 175

Met Thr Leu Thr Met Leu Ala Asn Phe Val Pro Leu Thr Leu Thr Leu
180 185 190

Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
225 230 235 240

Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu
245 250 255

Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro
260 265 270

Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
275 280 285

Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp Arg
 290 295 300

Ser Leu Arg Leu
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<210> 18
 <211> 926
 <212> DNA
 <213> Homo sapiens

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<210> 19
 <211> 298
 <212> PRT
 <213> Homo sapiens

<400> 19

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Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln Ile Leu
 35 40 45

Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe
 50 55 60

Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val
 65 70 75 80

Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met
 85 90 95

Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val
 115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
 130 135 140

Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln
 245 250 255

Ser Lys Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro
 260 265 270

Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Met Thr
 290 295

<210> 20
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 <212> DNA
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<210> 21
 <211> 309
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<400> 21

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Ile Ala Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile
 35 40 45

Ala Ala Leu Ala Val Ser Lys Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60

His Trp Tyr Ser Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val
 65 70 75 80

Ile Ile Phe Ile Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
 85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
 100 105 110

Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
 115 120 125

Val Leu Val Ile Val Leu Gly Ser Leu Phe Phe Leu Val Cys His Leu
 130 135 140

Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Glu Glu Cys Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Met His Leu Ser Asn
 165 170 175

Leu Thr Val Ala Met Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
 180 185 190

Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Ile His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Ile Leu Leu Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Leu Ile Ile Ser Phe Trp Asn Phe Lys Met Arg Pro
 245 250 255

Lys Glu Ile Val Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro
 260 265 270

Ser Phe His Ser Phe Ile Leu Ile Trp Gly Asn Lys Thr Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Val Thr Cys Trp Ala Lys Gly Gln
 290 295 300

Asn Gln Ser Thr Pro
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<210> 22
 <211> 927
 <212> DNA
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<210> 23
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 23

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Phe Val Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Phe
 20 25 30

Ile Asp Trp Val Lys Arg Lys Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu
 50 55 60

Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
 65 70 75 80

Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met
 85 90 95

Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val
 115 120 125

Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu
 130 135 140

Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly
 145 150 155 160

Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr
 165 170 175

Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Tyr Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
 245 250 255

Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
 260 265 270

Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
 275 280 285

Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
 290 295

<210> 24
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 <212> DNA
 <213> Homo sapiens

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 gcattattat taaattggta tttaactgtg ttgaatccag ctttttatag tgtagaatta 240

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agaattactt cttataatgc ctgggttgta accaaccatt tcagcatgtg gcttgctgct 300
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<210> 25

<211> 299

<212> PRT

<213> Homo sapiens

<400> 25

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Phe Leu Leu Gly Ile Phe Thr Asn Gly Ile Ile Val Val Val Asn Gly
20           25           30

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Ile Asp Leu Ile Lys His Arg Lys Met Ala Pro Leu Asp Leu Leu Leu
35           40           45

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Ser Cys Leu Ala Val Ser Arg Ile Phe Leu Gln Leu Phe Ile Phe Tyr
50           55           60

```

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Val Asn Val Ile Val Ile Phe Phe Ile Glu Phe Ile Met Cys Ser Ala
65           70           75           80

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Asn Cys Ala Ile Leu Leu Phe Ile Asn Glu Leu Glu Leu Trp Leu Ala
85           90           95

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Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Val Ala Ser Val Arg His
100          105          110

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Pro Leu Phe Ile Trp Leu Lys Met Arg Ile Ser Lys Leu Val Pro Trp
 115 120 125

Met Ile Leu Gly Ser Leu Leu Tyr Val Ser Met Ile Cys Val Phe His
 130 135 140

Ser Lys Tyr Ala Gly Phe Met Val Pro Tyr Phe Leu Arg Lys Phe Phe
 145 150 155 160

Ser Gln Asn Ala Thr Ile Gln Lys Glu Asp Thr Leu Ala Ile Gln Ile
 165 170 175

Phe Ser Phe Val Ala Glu Phe Ser Val Pro Leu Leu Ile Phe Leu Phe
 180 185 190

Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met
 195 200 205

Arg Asn Thr Val Ala Gly Ser Arg Val Pro Gly Arg Gly Ala Pro Ile
 210 215 220

Ser Ala Leu Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Phe Ser His
 225 230 235 240

Cys Met Ile Lys Val Phe Leu Ser Ser Leu Lys Phe His Ile Arg Arg
 245 250 255

Phe Ile Phe Leu Phe Phe Ile Leu Val Ile Gly Ile Tyr Pro Ser Gly
 260 265 270

His Ser Leu Ile Leu Ile Leu Gly Asn Pro Lys Leu Lys Gln Asn Ala
 275 280 285

Lys Lys Phe Leu Leu His Ser Lys Cys Cys Gln
 290 295

<210> 26
 <211> 897
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 <213> Homo sapiens

<400> 26

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<210> 27
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<212> PRT
<213> Homo sapiens

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<400> 27

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Met Leu Arg Leu Phe Tyr Phe Ser Ala Ile Ile Ala Ser Val Ile Leu
1           5           10          15

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Asn Phe Val Gly Ile Ile Met Asn Leu Phe Ile Thr Val Val Asn Cys
20           25           30

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Lys Thr Trp Val Lys Ser His Arg Ile Ser Ser Ser Asp Arg Ile Leu
35           40           45

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Phe Ser Leu Gly Ile Thr Arg Phe Leu Met Leu Gly Leu Phe Leu Val
50           55           60

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Asn Thr Ile Tyr Phe Val Ser Ser Asn Thr Glu Arg Ser Val Tyr Leu
65           70           75           80

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Ser Ala Phe Phe Val Leu Cys Phe Met Phe Leu Asp Ser Ser Ser Val
85 90 95

Trp Phe Val Thr Leu Leu Asn Ile Leu Tyr Cys Val Lys Ile Thr Asn
100 105 110

Phe Gln His Ser Val Phe Leu Leu Leu Lys Arg Asn Ile Ser Pro Lys
115 120 125

Ile Pro Arg Leu Leu Leu Ala Cys Val Leu Ile Ser Ala Phe Thr Thr
130 135 140

Cys Leu Tyr Ile Thr Leu Ser Gln Ala Ser Pro Phe Pro Glu Leu Val
145 150 155 160

Thr Thr Arg Asn Asn Thr Ser Phe Asn Ile Ser Glu Gly Ile Leu Ser
165 170 175

Leu Val Val Ser Leu Val Leu Ser Ser Ser Leu Gln Phe Ile Ile Asn
180 185 190

Val Thr Ser Ala Ser Leu Leu Ile His Ser Leu Arg Arg His Ile Gln
195 200 205

Lys Met Gln Lys Asn Ala Thr Gly Phe Trp Asn Pro Gln Thr Glu Ala
210 215 220

His Val Gly Ala Met Lys Leu Met Val Tyr Phe Leu Ile Leu Tyr Ile
225 230 235 240

Pro Tyr Ser Val Ala Thr Leu Val Gln Tyr Leu Pro Phe Tyr Ala Gly
245 250 255

Met Asp Met Gly Thr Lys Ser Ile Cys Leu Ile Phe Ala Thr Leu Tyr
260 265 270

Ser Pro Gly His Ser Val Leu Ile Ile Ile Thr His Pro Lys Leu Lys
275 280 285

Thr Thr Ala Lys Lys Ile Leu Cys Phe Lys Lys
290 295

<210> 28
 <211> 897
 <212> DNA
 <213> Homo sapiens

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<210> 29
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 29

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Phe Leu Ile Gly Leu Ile Gly Asn Gly Ser Leu Val Val Trp Ser Phe
 20 25 30

Arg Glu Trp Ile Arg Lys Phe Asn Trp Ser Ser Tyr Asn Leu Ile Ile
 35 40 45

Leu Gly Leu Ala Gly Cys Arg Phe Leu Leu Gln Trp Leu Ile Ile Leu
 50 55 60

Asp Leu Ser Leu Phe Pro Leu Phe Gln Ser Ser Arg Trp Leu Arg Tyr
 65 70 75 80

Leu Ser Ile Phe Trp Val Leu Val Ser Gln Ala Ser Leu Trp Phe Ala
 85 90 95

Thr Phe Leu Ser Val Phe Tyr Cys Lys Lys Ile Thr Thr Phe Asp Arg
 100 105 110

Pro Ala Tyr Leu Trp Leu Lys Gln Arg Ala Tyr Asn Leu Ser Leu Trp
 115 120 125

Cys Leu Leu Gly Tyr Phe Ile Ile Asn Leu Leu Leu Thr Val Gln Ile
 130 135 140

Gly Leu Thr Phe Tyr His Pro Pro Gln Gly Asn Ser Ser Ile Arg Tyr
 145 150 155 160

Pro Phe Glu Ser Trp Gln Tyr Leu Tyr Ala Phe Gln Leu Asn Ser Gly
 165 170 175

Ser Tyr Leu Pro Leu Val Val Phe Leu Val Ser Ser Gly Met Leu Ile
 180 185 190

Val Ser Leu Tyr Thr His His Lys Lys Met Lys Val His Ser Ala Gly
 195 200 205

Arg Arg Asp Val Arg Ala Lys Ala His Ile Thr Ala Leu Lys Ser Leu
 210 215 220

Gly Cys Phe Leu Leu Leu His Leu Val Tyr Ile Met Ala Ser Pro Phe
 225 230 235 240

Ser Ile Thr Ser Lys Thr Tyr Pro Pro Asp Leu Thr Ser Val Phe Ile
 245 250 255

Trp Glu Thr Leu Met Ala Ala Tyr Pro Ser Leu His Ser Leu Ile Leu
 260 265 270

Ile Met Gly Ile Pro Arg Val Lys Gln Thr Cys Gln Lys Ile Leu Trp
 275 280 285

Lys Thr Val Cys Ala Arg Arg Cys Trp Gly Pro
 290 295

<210> 30
 <211> 897
 <212> DNA
 <213> Homo sapiens

<400> 30
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 tggtcctcat ataacctcat tatcctgggc ctggctggct gccgatttct cctgcagtgg 180
 ctgatcattt tggacttaag cttgtttcca cttttccaga gcagccgttg gcttcgctat 240
 cttagtatct tctgggtcct ggtaagccag gccagcttat ggtttgccac cttcctcagt 300
 gtcttctatt gcaagaagat cacgaccttc gatcgcccgg cctacttggtg gctgaagcag 360
 agggcctata acctgagtct ctgggtgcctt ctgggctact ttataatcaa tttgttactt 420
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 ccctttgaaa gctggcagta cctgtatgca tttcagctca attcaggaag ttatttgcct 540
 ttagtggtgt ttcttgtttc ctctgggatg ctgattgtct ctttgatac acaccacaag 600
 aagatgaagg tccattcagc tggtaggagg gatgtccggg ccaaggctca catcactgcg 660
 ctgaagtctt tgggctgctt cctcttactt cacctggttt atatcatggc cagccccctt 720
 tccatcacct ccaagactta tcctcctgat ctcaccagtg tcttcatctg ggagacactc 780
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<210> 31
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 31

Met Ala Asp Lys Val Gln Thr Thr Leu Leu Phe Leu Ala Val Gly Glu
 1 5 10 15

Phe Ser Val Gly Ile Leu Gly Asn Ala Phe Ile Gly Leu Val Asn Cys
 20 25 30

Met Asp Trp Val Lys Lys Arg Lys Ile Ala Ser Ile Asp Leu Ile Leu
 35 40 45

Thr Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Leu Leu
 50 55 60

Asp Cys Phe Ile Leu Val Leu Tyr Pro Asp Val Tyr Ala Thr Gly Lys
 65 70 75 80

Glu Met Arg Ile Ile Asp Phe Phe Trp Thr Leu Thr Asn His Leu Ser
 85 90 95

Ile Trp Phe Ala Thr Cys Leu Ser Ile Tyr Tyr Phe Phe Lys Ile Gly
 100 105 110

Asn Phe Phe His Pro Leu Phe Leu Trp Met Lys Trp Arg Ile Asp Arg
 115 120 125

Val Ile Ser Trp Ile Leu Leu Gly Cys Val Val Leu Ser Val Phe Ile
 130 135 140

Ser Leu Pro Ala Thr Glu Asn Leu Asn Ala Asp Phe Arg Phe Cys Val
 145 150 155 160

Lys Ala Lys Arg Lys Thr Asn Leu Thr Trp Ser Cys Arg Val Asn Lys
 165 170 175

Thr Gln His Ala Ser Thr Lys Leu Phe Leu Asn Leu Ala Thr Leu Leu
 180 185 190

Pro Phe Cys Val Cys Leu Met Ser Phe Phe Leu Leu Ile Leu Ser Leu
 195 200 205

Arg Arg His Ile Arg Arg Met Gln Leu Ser Ala Thr Gly Cys Arg Asp
 210 215 220

Pro Ser Thr Glu Ala His Val Arg Ala Leu Lys Ala Val Ile Ser Phe
 225 230 235 240

Leu Leu Leu Phe Ile Ala Tyr Tyr Leu Ser Phe Leu Ile Ala Thr Ser
 245 250 255

Ser Tyr Phe Met Pro Glu Thr Glu Leu Ala Val Ile Phe Gly Glu Ser
 260 265 270

Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly
 275 280 285

Asn Asn Lys Leu Arg His Ala Ser Leu Lys Val Ile Trp Lys Val Met
 290 295 300

Ser Ile Leu Lys Gly Arg Lys Phe Gln Gln His Lys Gln Ile
 305 310 315

<210> 32
 <211> 954
 <212> DNA
 <213> Homo sapiens

<400> 32
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 attgcctcca ttgatttaat ctcacaagt ctggccatat ccagaatttg tctattgtgc 180
 gtaatactat tagattgttt tatattggtg ctatatccag atgtctatgc cactggtaaa 240
 gaaatgagaa tcattgactt cttctggaca ctaaccaatc atttaagtat ctggtttgca 300
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 tggatgaagt ggagaattga cagggtgatt tcctggattc tactggggtg cgtggttctc 420
 tctgtgttta ttagccttcc agccactgag aatttgaacg ctgatttcag gttttgtgtg 480
 aaggcaaaga ggaaaacaaa cttaacttgg agttgcagag taaataaaac tcaacatgct 540
 tctaccaagt tatttctcaa cctggcaacg ctgctcccct tttgtgtgtg cctaattgtc 600
 ttttctctct tgatcctctc cctgcggaga catatcaggc gaatgcagct cagtgccaca 660
 ggggtgcagag accccagcac agaagcccat gtgagagccc tgaaagctgt catttccttc 720
 cttctctctt ttattgccta ctatttgtcc tttctcattg ccacctccag ctactttatg 780
 ccagagacgg aattagctgt gatttttggg gagtccatag ctctaatac cccctcaagt 840

cattcattta tcctaatact ggggaacaat aaattaagac atgcatctct aaaggtgatt 900
 tggaaagtaa tgtctattct aaaaggaaga aaattccaac aacataaaca aatc 954

<210> 33
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 33

Met	Phe	Ser	Pro	Ala	Asp	Asn	Ile	Phe	Ile	Ile	Leu	Ile	Thr	Gly	Glu	
1				5					10					15		
Phe	Ile	Leu	Gly	Ile	Leu	Gly	Asn	Gly	Tyr	Ile	Ala	Leu	Val	Asn	Trp	
			20					25					30			
Ile	Asp	Trp	Ile	Lys	Lys	Lys	Lys	Ile	Ser	Thr	Val	Asp	Tyr	Ile	Leu	
		35					40					45				
Thr	Asn	Leu	Val	Ile	Ala	Arg	Ile	Cys	Leu	Ile	Ser	Val	Met	Val	Val	
		50				55					60					
Asn	Gly	Ile	Val	Ile	Val	Leu	Asn	Pro	Asp	Val	Tyr	Thr	Lys	Asn	Lys	
65					70					75				80		
Gln	Gln	Ile	Val	Ile	Phe	Thr	Phe	Trp	Thr	Phe	Ala	Asn	Tyr	Leu	Asn	
			85						90					95		
Met	Trp	Ile	Thr	Thr	Cys	Leu	Asn	Val	Phe	Tyr	Phe	Leu	Lys	Ile	Ala	
			100					105					110			
Ser	Ser	Ser	His	Pro	Leu	Phe	Leu	Trp	Leu	Lys	Trp	Lys	Ile	Asp	Met	
		115					120					125				
Val	Val	His	Trp	Ile	Leu	Leu	Gly	Cys	Phe	Ala	Ile	Ser	Leu	Leu	Val	
		130				135					140					
Ser	Leu	Ile	Ala	Ala	Ile	Val	Leu	Ser	Cys	Asp	Tyr	Arg	Phe	His	Ala	
145					150					155				160		
Ile	Ala	Lys	His	Lys	Arg	Asn	Ile	Thr	Glu	Met	Phe	His	Val	Ser	Lys	
				165					170					175		

Ile Pro Tyr Phe Glu Pro Leu Thr Leu Phe Asn Leu Phe Ala Ile Val
 180 185 190

Pro Phe Ile Val Ser Leu Ile Ser Phe Phe Leu Leu Val Arg Ser Leu
 195 200 205

Trp Arg His Thr Lys Gln Ile Lys Leu Tyr Ala Thr Gly Ser Arg Asp
 210 215 220

Pro Ser Thr Glu Val His Val Arg Ala Ile Lys Thr Met Thr Ser Phe
 225 230 235 240

Ile Phe Phe Phe Phe Leu Tyr Tyr Ile Ser Ser Ile Leu Met Thr Phe
 245 250 255

Ser Tyr Leu Met Thr Lys Tyr Lys Leu Ala Val Glu Phe Gly Glu Ile
 260 265 270

Ala Ala Ile Leu Tyr Pro Leu Gly His Ser Leu Ile Leu Ile Val Leu
 275 280 285

Asn Asn Lys Leu Arg Gln Thr Phe Val Arg Met Leu Thr Cys Arg Lys
 290 295 300

Ile Ala Cys Met Ile
 305

<210> 34
 <211> 927
 <212> DNA
 <213> Homo sapiens

<400> 34
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 atttccacag ttgactacat cttaccaat ttagttatcg ccagaatttg tttgatcagt 180
 gtaatgggtg taaatggcat tgtaatagta ctgaaccag atgtttatac aaaaaataaa 240
 caacagatag tcattttttac cttctggaca ttgccaact acttaaatat gtggattacc 300
 acctgcctta atgtcttcta ttttctgaag atagccagtt cctctcatcc actttttctc 360
 tggctgaagt ggaaaattga tatggtggtg cactggatcc tgctgggatg ctttgccatt 420

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tccttggttg tcagccttat agcagcaata gtactgagtt gtgattatag gtttcatgca 480
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gaacccttaa ctctctttta cctgtttgca attgtcccat ttattgtgtc actgatatca 600
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ggcagtagag accccagcac agaagttcat gtgagagcca ttaaaaactat gacttcattt 720
atcttctttt ttttctata ctatatttct tctattttga tgacctttag ctatcttatg 780
acaaaatata agttagctgt ggagtttgga gagattgcag caattctcta ccccttgggt 840
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acatgtagaa aaattgcctg catgata 927

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<210> 35
<211> 312
<212> PRT
<213> Homo sapiens

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<400> 35
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Met Pro Ser Ala Ile Glu Ala Ile Tyr Ile Ile Leu Ile Ala Gly Glu
1           5           10          15

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Leu Thr Ile Gly Ile Trp Gly Asn Gly Phe Ile Val Leu Val Asn Cys
          20          25          30

```

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Ile Asp Trp Leu Lys Arg Arg Asp Ile Ser Leu Ile Asp Ile Ile Leu
          35          40          45

```

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Ile Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Ser Leu
          50          55          60

```

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Asp Gly Phe Phe Met Leu Leu Phe Pro Gly Thr Tyr Gly Asn Ser Val
65          70          75          80

```

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Leu Val Ser Ile Val Asn Val Val Trp Thr Phe Ala Asn Asn Ser Ser
          85          90          95

```

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Leu Trp Phe Thr Ser Cys Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
          100          105          110

```

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Asn Ile Ser His Pro Phe Phe Phe Trp Leu Lys Leu Lys Ile Asn Lys
          115          120          125

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Val Met Leu Ala Ile Leu Leu Gly Ser Phe Leu Ile Ser Leu Ile Ile
 130 135 140

Ser Val Pro Lys Asn Asp Asp Met Trp Tyr His Leu Phe Lys Val Ser
 145 150 155 160

His Glu Glu Asn Ile Thr Trp Lys Phe Lys Val Ser Lys Ile Pro Gly
 165 170 175

Thr Phe Lys Gln Leu Thr Leu Asn Leu Gly Val Met Val Pro Phe Ile
 180 185 190

Leu Cys Leu Ile Ser Phe Phe Leu Leu Leu Phe Ser Leu Val Arg His
 195 200 205

Thr Lys Gln Ile Arg Leu His Ala Thr Gly Phe Arg Asp Pro Ser Thr
 210 215 220

Glu Ala His Met Arg Ala Ile Lys Ala Val Ile Ile Phe Leu Leu Leu
 225 230 235 240

Leu Ile Val Tyr Tyr Pro Val Phe Leu Val Met Thr Ser Ser Ala Leu
 245 250 255

Ile Pro Gln Gly Lys Leu Val Leu Met Ile Gly Asp Ile Val Thr Val
 260 265 270

Ile Phe Pro Ser Ser His Ser Phe Ile Leu Ile Met Gly Asn Ser Lys
 275 280 285

Leu Arg Glu Ala Phe Leu Lys Met Leu Arg Phe Val Lys Cys Phe Leu
 290 295 300

Arg Arg Arg Lys Pro Phe Val Pro
 305 310

<210> 36
 <211> 936
 <212> DNA
 <213> Homo sapiens

<400> 36


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atttccttga ttgacatcat cctgatcagc ttggccatct ccagaatctg tctgctgtgt     180
gtaatatcat tagatggctt ctttatgctg ctctttccag gtacatatgg caatagcgtg     240
ctagtaagca ttgtgaatgt tgtctggaca ttgccaata attcaagtct ctggtttact     300
tcttgccctca gtatcttcta tttactcaag atagccaata tatcgacacc atttttcttc     360
tggctgaagc taaagatcaa caaggtcatg cttgcgattc ttctgggggc ctttcttacc     420
tctttaatta ttagtggtcc aaagaatgat gatatgtggt atcacctttt caaagtcagt     480
catgaagaaa acattacttg gaaattcaaa gtgagtaaaa ttccaggtag tttcaaacag     540
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ttacttttct ccctagttag acacaccaag cagattcgac tgcattgctac agggttcaga     660
gacccagta cagaggcca catgagggcc ataaaggcag tgatcatctt tctgctctc     720
ctcatcgtgt actaccagt ctttcttggt atgacctcta gcgctctgat tcctcaggga     780
aaattagtgt tgatgattgg tgacatagta actgtcattt tcccatcaag ccattcattc     840
attctaatta tgggaaatag caagttgagg gaagcttttc tgaagatggt aagatttggt     900
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<210> 37
<211> 307
<212> PRT
<213> Homo sapiens

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<400> 37

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Met Leu Arg Val Val Glu Gly Ile Phe Ile Phe Val Val Val Ser Glu
1           5           10          15

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Ser Val Phe Gly Val Leu Gly Asn Gly Phe Ile Gly Leu Val Asn Cys
          20           25           30

```

```

Ile Asp Cys Ala Lys Asn Lys Leu Ser Thr Ile Gly Phe Ile Leu Thr
          35           40           45

```

```

Gly Leu Ala Ile Ser Arg Ile Phe Leu Ile Trp Ile Ile Ile Thr Asp
          50           55           60

```

Gly Phe Ile Gln Ile Phe Ser Pro Asn Ile Tyr Ala Ser Gly Asn Leu
65 70 75 80

Ile Glu Tyr Ile Ser Tyr Phe Trp Val Ile Gly Asn Gln Ser Ser Met
85 90 95

Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Tyr Ile Phe Leu Trp Leu Lys Ser Arg Thr Asn Met Val
115 120 125

Leu Pro Phe Met Ile Val Phe Leu Leu Ile Ser Ser Leu Leu Asn Phe
130 135 140

Ala Tyr Ile Ala Lys Ile Leu Asn Asp Tyr Lys Met Lys Asn Asp Thr
145 150 155 160

Val Trp Asp Leu Asn Met Tyr Lys Ser Glu Tyr Phe Ile Lys Gln Ile
165 170 175

Leu Leu Asn Leu Gly Val Ile Phe Phe Phe Thr Leu Ser Leu Ile Thr
180 185 190

Cys Ile Phe Leu Ile Ile Ser Leu Trp Arg His Asn Arg Gln Met Gln
195 200 205

Ser Asn Val Thr Gly Leu Arg Asp Ser Asn Thr Glu Ala His Val Lys
210 215 220

Ala Met Lys Val Leu Ile Ser Phe Ile Ile Leu Phe Ile Leu Tyr Phe
225 230 235 240

Ile Gly Met Ala Ile Glu Ile Ser Cys Phe Thr Val Arg Glu Asn Lys
245 250 255

Leu Leu Leu Met Phe Gly Met Thr Thr Thr Ala Ile Tyr Pro Trp Gly
260 265 270

His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Ala Ser
275 280 285

Leu Arg Val Leu Gln Gln Leu Lys Cys Cys Glu Lys Arg Lys Asn Leu
 290 295 300

Arg Val Thr
 305

<210> 38
 <211> 921
 <212> DNA
 <213> Homo sapiens

<400> 38
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 tctacgattg gctttattct caccggctta gctatttcaa gaatttttct gatatggata 180
 ataattacag atggatttat acagatatcc tctccaaata tatatgcctc cggtaaccta 240
 attgaatata ttagttactt ttgggtaatt ggtaatcaat caagtatgtg gtttgccacc 300
 agcctcagca tcttctatct cctgaagata gcaaattttt ccaactacat atttctctgg 360
 ttgaagagca gaacaaatat ggttcttccc ttcattgatag tattcttact tatttcacgc 420
 ttacttaatt ttgcatacat tgccaagatt cttaatgatt ataaaatgaa gaatgacaca 480
 gtctgggagc tcaacatgta taaaagttaa tactttatta aacagatttt gctaaatctg 540
 ggagtcattt tcttctttac actatcccta attacatgta tttttttaat catttccctt 600
 tggagacaca acaggcagat gcaatcgaat gtgacaggat tgagagactc caacacagaa 660
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 tttggaatga caaccacagc catctatccc tggggtcact catttatctt aattctagga 840
 aacagcaagc taaagcaagc ctctttgagg gtactgcagc aattgaagtg ctgtgagaaa 900
 aggaaaaatc tcagagtcac a 921

<210> 39
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 39

Met Glu Ser Ala Leu Pro Ser Ile Phe Thr Leu Val Ile Ile Ala Glu
 1 5 10 15

Phe Ile Ile Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ile Asn Cys
 20 25 30

Ile Asp Trp Val Ser Lys Arg Glu Leu Ser Ser Val Asp Lys Leu Leu
 35 40 45

Ile Ile Leu Ala Ile Ser Arg Ile Gly Leu Ile Trp Glu Ile Leu Val
 50 55 60

Ser Trp Phe Leu Ala Leu His Tyr Leu Ala Ile Phe Val Ser Gly Thr
 65 70 75 80

Gly Leu Arg Ile Met Ile Phe Ser Trp Ile Val Ser Asn His Phe Asn
 85 90 95

Leu Trp Leu Ala Thr Ile Phe Ser Ile Phe Tyr Leu Leu Lys Ile Ala
 100 105 110

Ser Phe Ser Ser Pro Ala Phe Leu Tyr Leu Lys Trp Arg Val Asn Lys
 115 120 125

Val Ile Leu Met Ile Leu Leu Gly Thr Leu Val Phe Leu Phe Leu Asn
 130 135 140

Leu Ile Gln Ile Asn Met His Ile Lys Asp Trp Leu Asp Arg Tyr Glu
 145 150 155 160

Arg Asn Thr Thr Trp Asn Phe Ser Met Ser Asp Phe Glu Thr Phe Ser
 165 170 175

Val Ser Val Lys Phe Thr Met Thr Met Phe Ser Leu Thr Pro Phe Thr
 180 185 190

Val Ala Phe Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Gln Lys His
 195 200 205

Leu Gln Lys Met Gln Leu Asn Tyr Lys Gly His Arg Asp Pro Arg Thr
 210 215 220

Lys Val His Thr Asn Ala Leu Lys Ile Val Ile Ser Phe Leu Leu Phe
 225 230 235 240

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<210> 41
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 41

Met Gly Gly Val Ile Lys Ser Ile Phe Thr Phe Val Leu Ile Val Glu
 1 5 10 15

Phe Ile Ile Gly Asn Leu Gly Asn Ser Phe Ile Ala Leu Val Asn Cys
 20 25 30

Ile Asp Trp Val Lys Gly Arg Lys Ile Ser Ser Val Asp Arg Ile Leu
 35 40 45

Thr Ala Leu Ala Ile Ser Arg Ile Ser Leu Val Trp Leu Ile Phe Gly
 50 55 60

Ser Trp Cys Val Ser Val Phe Phe Pro Ala Leu Phe Ala Thr Glu Lys
 65 70 75 80

Met Phe Arg Met Leu Thr Asn Ile Trp Thr Val Ile Asn His Phe Ser
 85 90 95

Val Trp Leu Ala Thr Gly Leu Gly Thr Phe Tyr Phe Leu Lys Ile Ala
 100 105 110

Asn Phe Ser Asn Ser Ile Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys
 115 120 125

Val Val Leu Val Leu Leu Leu Val Thr Ser Val Phe Leu Phe Leu Asn
 130 135 140

Ile Ala Leu Ile Asn Ile His Ile Asn Ala Ser Ile Asn Gly Tyr Arg
 145 150 155 160

Arg Asn Lys Thr Cys Ser Ser Asp Ser Ser Asn Phe Thr Arg Phe Ser
 165 170 175

Ser Leu Ile Val Leu Thr Ser Thr Val Phe Ile Phe Ile Pro Phe Thr
 180 185 190

Leu Ser Leu Ala Met Phe Leu Leu Leu Ile Phe Ser Met Trp Lys His
 195 200 205

Arg Lys Lys Met Gln His Thr Val Lys Ile Ser Gly Asp Ala Ser Thr
 210 215 220

Lys Ala His Arg Gly Val Lys Ser Val Ile Thr Phe Phe Leu Leu Tyr
 225 230 235 240

Ala Ile Phe Ser Leu Ser Phe Phe Ile Ser Val Trp Thr Ser Glu Arg
 245 250 255

Leu Glu Glu Asn Leu Ile Ile Leu Ser Gln Val Met Gly Met Ala Tyr
 260 265 270

Pro Ser Cys His Ser Cys Val Leu Ile Leu Gly Asn Lys Lys Leu Arg
 275 280 285

Gln Ala Ser Leu Ser Val Leu Leu Trp Leu Arg Tyr Met Phe Lys Asp
 290 295 300

Gly Glu Pro Ser Gly His Lys Glu Phe Arg Glu Ser Ser
 305 310 315

<210> 42
 <211> 951
 <212> DNA
 <213> Homo sapiens

<400> 42
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 ttaatatctg gaagctggtg tgtgtctgtg tttttcccag ctttatttgc cactgaaaaa 240
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 acaggcctcg gtacttttta ttttctcaag atagccaatt tttctaactc tatttttctc 360
 tacctaaagt ggagagttaa aaaggtggtt ttggtgctgc ttcttgtagc ttcggtcttc 420
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 agaaacaaga cttgcagttc tgattcaagt aactttacac gattttccag tcttattgta 540

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gacgccagca ccaaagccca cagaggagtt aaaagtgtga tcactttctt cctactctat 720
gccattttct ctctgtcttt tttcatatca gtttggacct ctgaaagggt ggaggaaaat 780
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<210> 43
<211> 291
<212> PRT
<213> Homo sapiens

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<400> 43

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Met Ile Pro Ile Gln Leu Thr Val Phe Phe Met Ile Ile Tyr Val Leu
1             5             10             15

```

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Glu Ser Leu Thr Ile Ile Val Gln Ser Ser Leu Ile Val Ala Val Leu
20             25             30

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Gly Arg Glu Trp Leu Gln Val Arg Arg Leu Met Pro Val Asp Met Ile
35             40             45

```

```

Leu Ile Ser Leu Gly Ile Ser Arg Phe Cys Leu Gln Trp Ala Ser Met
50             55             60

```

```

Leu Asn Asn Phe Cys Ser Tyr Phe Asn Leu Asn Tyr Val Leu Cys Asn
65             70             75             80

```

```

Leu Thr Ile Thr Trp Glu Phe Phe Asn Ile Leu Thr Phe Trp Leu Asn
85             90             95

```

```

Ser Leu Leu Thr Val Phe Tyr Cys Ile Lys Val Ser Ser Phe Thr His
100            105            110

```

```

His Ile Phe Leu Trp Leu Arg Trp Arg Ile Leu Arg Leu Phe Pro Trp
115            120            125

```

```

Ile Leu Leu Gly Ser Leu Met Ile Thr Cys Val Thr Ile Ile Pro Ser
130            135            140

```


Ala Ile Gly Asn Tyr Ile Gln Ile Gln Leu Leu Thr Met Glu His Leu
 145 150 155 160

Pro Arg Asn Ser Thr Val Thr Asp Lys Leu Glu Asn Phe His Gln Tyr
 165 170 175

Gln Phe Gln Ala His Thr Val Ala Leu Val Ile Pro Phe Ile Leu Phe
 180 185 190

Leu Ala Ser Thr Ile Phe Leu Met Ala Ser Leu Thr Lys Gln Ile Gln
 195 200 205

His His Ser Thr Gly His Cys Asn Pro Ser Met Lys Ala His Phe Thr
 210 215 220

Ala Leu Arg Ser Leu Ala Val Leu Phe Ile Val Phe Thr Ser Tyr Phe
 225 230 235 240

Leu Thr Ile Leu Ile Thr Ile Ile Gly Thr Leu Phe Asp Lys Arg Cys
 245 250 255

Trp Leu Trp Val Trp Glu Ala Phe Val Tyr Ala Phe Ile Leu Met His
 260 265 270

Ser Thr Ser Leu Met Leu Ser Ser Pro Thr Leu Lys Arg Ile Leu Lys
 275 280 285

Gly Lys Cys
 290

<210> 44
 <211> 873
 <212> DNA
 <213> Homo sapiens

<400> 44
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 attattgtgc agagcagcct aattgttgca gtgctgggca gagaatggct gcaagtcaga 120
 aggctgatgc ctgtggacat gattctcatc agcctgggca tctctcgctt ctgtctacag 180
 tgggcatcaa tgctgaacaa tttttgctcc tattttaatt tgaattatgt actttgcaac 240

```

ttaacaatca cctgggaatt ttttaatatc cttacattct ggttaaacag cttgcttacc 300
gtgtttctact gcatcaaggt ctcttctttc acccatcaca tctttctctg gctgaggtgg 360
agaatthtga ggttgthtcc ctggatatta ctgggttctc tgatgattac ttgtgtaaca 420
atcatccctt cagctattgg gaattacatt caaattcagt tactcaccat ggagcatcta 480
ccaagaaaca gcactgtaac tgacaaactt gaaaattttc atcagtatca gttccaggct 540
catacagttg cattggttat tcctttcatc ctgttctctg cctccaccat ctttctcatg 600
gcatcactga ccaagcagat acaacatcat agcactgggc actgcaatcc aagcatgaaa 660
gcgcacttca ctgccctgag gtcccttgcc gtcttattta ttgtgtttac ctcttacttt 720
ctaaccatac tcatcaccat tataggtact ctatttgata agagatgttg gttatgggtc 780
tggaagctt ttgtctatgc tttcatctta atgcattcca cttcactgat gctgagcagc 840
cctacgttga aaaggattct aaagggaag tgc 873

```

```

<210> 45
<211> 316
<212> PRT
<213> Homo sapiens

```

```
<400> 45
```

```

Met Met Gly Leu Thr Glu Gly Val Phe Leu Ile Leu Ser Gly Thr Gln
1           5           10           15

```

```

Phe Thr Leu Gly Ile Leu Val Asn Cys Phe Ile Glu Leu Val Asn Gly
20           25           30

```

```

Ser Ser Trp Phe Lys Thr Lys Arg Met Ser Leu Ser Asp Phe Ile Ile
35           40           45

```

```

Thr Thr Leu Ala Leu Leu Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr
50           55           60

```

```

Asp Ser Phe Leu Ile Glu Phe Ser Pro Asn Thr His Asp Ser Gly Ile
65           70           75           80

```

```

Ile Met Gln Ile Ile Asp Val Ser Trp Thr Phe Thr Asn His Leu Ser
85           90           95

```

```

Ile Trp Leu Ala Thr Cys Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala
100          105          110

```

Ser Phe Ser His Pro Thr Phe Leu Trp Leu Lys Trp Arg Val Ser Arg
 115 120 125

Val Met Val Trp Met Leu Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser
 130 135 140

Thr Ala Ser Leu Ile Asn Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly
 145 150 155 160

Ile Glu Ala Thr Arg Asn Val Thr Glu His Phe Arg Lys Lys Arg Ser
 165 170 175

Glu Tyr Tyr Leu Ile His Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro
 180 185 190

Leu Ile Val Ser Leu Ala Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly
 195 200 205

Arg His Thr Arg Gln Met Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro
 210 215 220

Thr Thr Glu Ala His Lys Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe
 225 230 235 240

Phe Leu Phe Leu Leu Tyr Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly
 245 250 255

Asn Phe Leu Pro Lys Thr Lys Met Ala Lys Met Ile Gly Glu Val Met
 260 265 270

Thr Met Phe Tyr Pro Ala Gly His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285

Ser Lys Leu Lys Gln Thr Phe Val Val Met Leu Arg Cys Glu Ser Gly
 290 295 300

His Leu Lys Pro Gly Ser Lys Gly Pro Ile Phe Ser
 305 310 315

<210> 46

<211> 948

<212> DNA

<213> Homo sapiens

<400> 46

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atgatgggac tcaccgaggg ggtgttcctg attctgtctg gcactcagtt cacactggga      60
attctgggtca attgtttcat tgagttgggtc aatggtagca gctgggtcaa gaccaagaga      120
atgtctttgt ctgacttcat catcaccacc ctggcactct tgaggatcat tctgctgtgt      180
attatcttga ctgatagttt tttaatagaa ttctctccca acacacatga ttcagggaata      240
ataatgcaaa ttattgatgt ttcttggaac ttacaaacc atctgagcat ttggcttgcc      300
acctgtcttg gtgtcctcta ctgcctgaaa atcgccagtt tctctcacc caccattctc      360
tggtctcaagt ggagagtttc taggggtgatg gtatggatgc tgttgggtgc actgctctta      420
tcctgtggta gtaccgcata tctgatcaat gagtttaagc tctattctgt ctttagggga      480
attgaggcca ccaggaatgt gactgaacac ttcagaaaga agaggagtga gtattatctg      540
atccatgttc ttgggactct gtggtacctg cctcccttaa ttgtgtcctt ggccctctac      600
tctttgtcga tcttctcctt ggggaggcac acacggcaga tgctgcaaaa tgggacaagc      660
tccagagatc caaccactga ggcccacaag agggccatca gaatcatcct ttccttcttc      720
tttctcttct tactttactt tcttgctttc ttaattgcat catttggtaa tttcctacca      780
aaaaccaaga tggctaagat gattggcgaa gtaatgacaa tgttttatcc tgctggccac      840
tcatttatcc tcattctggg gaacagtaag ctgaagcaga catttgtagt gatgctccgg      900
tgtgagtcctg gtcacttgaa gcctggatcc aagggaacca ttttctct      948

```

<210> 47

<211> 314

<212> PRT

<213> Homo sapiens

<400> 47

```

Met Ala Thr Glu Leu Asp Lys Ile Phe Leu Ile Leu Ala Ile Ala Glu
1           5           10          15

```

```

Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys
20           25           30

```

```

Ser Glu Gly Ile Lys Asn Gln Lys Val Phe Ser Ala Asp Phe Ile Leu
35           40           45

```

Thr Cys Leu Ala Ile Ser Thr Ile Gly Gln Leu Leu Val Ile Leu Phe
 50 55 60

Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg
 65 70 75 80

Leu Gly Lys Thr Val Ile Met Leu Trp His Met Thr Asn His Leu Thr
 85 90 95

Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
 100 105 110

His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly
 115 120 125

Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp
 130 135 140

Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp
 145 150 155 160

Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Phe Asp
 165 170 175

Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro
 180 185 190

Phe Ser Leu Ser Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val
 195 200 205

Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser
 210 215 220

Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu
 225 230 235 240

Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Trp Ile
 245 250 255

Phe Phe Met Leu Trp Asn Asn Lys Tyr Ile Lys Phe Val Met Leu Ala
 260 265 270

Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285

Ser Lys Leu Arg Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn
 290 295 300

Tyr Thr Lys Thr Pro Asn Ala Leu Pro Leu
 305 310

<210> 48
 <211> 942
 <212> DNA
 <213> Homo sapiens

<400> 48
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 gtcttctcag ctgacttcat cctcacctgc ttggctatct ccacaattgg acaactgttg 180
 gtgatactgt ttgattcatt tctagtggga cttgcttcac atttatatac cacatataga 240
 ctaggaaaaa ctgttattat gctttggcac atgactaatc acttgacaac ctggcttgcc 300
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 tggctgaggt ggaggatgaa cggaatgatt gttatgcttc ttatattgtc tttgttctta 420
 ctgatttttg acagtttagt gctagaaata tttattgata tctcactcaa tataatagat 480
 aaaagtaatc tgactttata tttagatgaa agtaaaactc tctttgataa actctctatt 540
 ttaaaaactc ttctcagctt gaccagtttt atcccccttt ctctgtccct gacctccttg 600
 ctttttttat ttctgtcctt ggtgagacat actagaaatt tgaagctcag ttccttgggc 660
 tctagagact ccagcacaga ggcccatagg agggccatga aaatggtgat gtctttcctt 720
 ttctcttca tagttcattt tttttcctta caagtggcca attggatatt ttttatgttg 780
 tggaacaaca agtacataaa gtttgtcatg ttagccttaa atgcctttcc ctctgtccac 840
 tcattttattc tcattctggg aaacagcaag ctgcgacaga cagctgtgag gctactgtgg 900
 catcttagga actatacaaa aacaccaa atgctttacctt tg 942

<210> 49
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 49

Met Asn Gly Asp His Met Val Leu Gly Ser Ser Val Thr Asp Lys Lys
 1 5 10 15

Ala Ile Ile Leu Val Thr Ile Leu Leu Leu Arg Leu Val Ala Ile
 20 25 30

Ala Gly Asn Gly Phe Ile Thr Ala Ala Leu Gly Val Glu Trp Val Leu
 35 40 45

Arg Arg Met Leu Leu Pro Cys Asp Lys Leu Leu Val Ser Leu Gly Ala
 50 55 60

Ser Arg Phe Cys Leu Gln Ser Val Val Met Gly Lys Thr Ile Tyr Val
 65 70 75 80

Phe Leu His Pro Met Ala Phe Pro Tyr Asn Pro Val Leu Gln Phe Leu
 85 90 95

Ala Phe Gln Trp Asp Phe Leu Asn Ala Ala Thr Leu Trp Ser Ser Thr
 100 105 110

Trp Leu Ser Val Phe Tyr Cys Val Lys Ile Ala Thr Phe Thr His Pro
 115 120 125

Val Phe Phe Trp Leu Lys His Lys Leu Ser Gly Trp Leu Pro Trp Met
 130 135 140

Leu Phe Ser Ser Val Gly Leu Ser Ser Phe Thr Thr Ile Leu Phe Phe
 145 150 155 160

Ile Gly Asn His Arg Met Tyr Gln Asn Tyr Leu Arg Asn His Leu Gln
 165 170 175

Pro Trp Asn Val Thr Gly Asp Ser Ile Arg Ser Tyr Cys Glu Lys Phe
 180 185 190

Tyr Leu Phe Pro Leu Lys Met Ile Thr Trp Thr Met Pro Thr Ala Val
 195 200 205

Phe Phe Ile Cys Met Ile Leu Leu Ile Thr Ser Leu Gly Arg His Arg
 210 215 220

Lys Lys Ala Leu Leu Thr Thr Ser Gly Phe Arg Glu Pro Ser Val Gln
 225 230 235 240

Ala His Ile Lys Ala Leu Leu Ala Leu Leu Ser Phe Ala Met Leu Phe
 245 250 255

Ile Ser Tyr Phe Leu Ser Leu Val Phe Ser Ala Ala Gly Ile Phe Pro
 260 265 270

Pro Leu Asp Phe Lys Phe Trp Val Trp Glu Ser Val Ile Tyr Leu Cys
 275 280 285

Ala Ala Val His Pro Ile Ile Leu Leu Phe Ser Asn Cys Arg Leu Arg
 290 295 300

Ala Val Leu Lys Ser Arg Arg Ser Ser Arg Cys Gly Thr Pro
 305 310 315

<210> 50
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 50
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 gctctggggc tggagtgggt gctacggaga atgttggtgc cttgtgataa gttattgggt 180
 agcctagggg cctctcgctt ctgtctgcag tcagtggtaa tgggtaagac catttatggt 240
 ttcttgcata cgatggcctt cccatacaac cctgtactgc agtttctagc tttccagtgg 300
 gacttctga atgctgccac cttatgggtc tctacctggc tcagtgtctt ctattgtgtg 360
 aaaattgcta ccttcacca cctgtcttc ttctggctaa agcacaagtt gtctgggtgg 420
 ctaccatgga tgctcttcag ctctgtaggg ctctccagct tcaccaccat tctatttttc 480
 ataggcaacc acagaatgta tcagaactat ttaaggaacc atctacaacc ttggaatgtc 540
 actggcgata gcatacggag ctactgtgag aaattctatc tcttcctctt aaaaatgatt 600
 acttggaaca tgcccactgc tgtctttttc atttgcatga ttttgctcat cacatctctg 660
 ggaagacaca ggaagaaggc tctccttaca acctcaggat tccgagagcc cagtgtgcag 720

gcacacataa aggctctgct ggctctcctc tcttttgcca tgctcttcat ctcataatttc 780
ctgtcactgg tgttcagtgc tgcaggtatt tttccacctc tggactttaa attctgggtg 840
tgaggagtcag tgatttatct gtgtgcagca gttcacccca tcattctgct cttcagcaac 900
tgcaggctga gagctgtgct gaagagtcgt cgttcctcaa ggtgtgggac accttga 957

<210> 51
<211> 33
<212> DNA
<213> Artificial

<220>

<223> Primer comprising EcoRI restriction site for PCR amplification of
hTAS2R16

<400> 51
cctgggaatt ttttaatatc cttacattct ggt 33

<210> 52
<211> 19
<212> DNA
<213> Artificial

<220>

<223> Primer comprising NotI restriction site for PCR amplification of
hTAS2R16

<400> 52
gaagcgcgct ttcattgctt 19